

13

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/538,198  
Source: PUF  
Date Processed by STIC: 2/16/06

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PCT

## RAW SEQUENCE LISTING

DATE: 02/16/2006

PATENT APPLICATION: US/10/538,198

TIME: 13:05:21

Input Set : A:\2005-12-23 0933-0247PUS1.ST25.txt

Output Set: N:\CRF4\02162006\J538198.raw

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3 <110> APPLICANT: SALONEN, Jukka T.
4     PIRSKANEN, Mia
5     TUOMAINEN, Tomi-Pekka
6     YUNUS, Faisal
8 <120> TITLE OF INVENTION: METHOD AND KIT FOR DETECTING A RISK OF DIABETES OR A
METABOLIC SYNDROME
10 <130> FILE REFERENCE: 0933-0247PUS1
12 <140> CURRENT APPLICATION NUMBER: US 10/538,198
13 <141> CURRENT FILING DATE: 2005-06-09
15 <150> PRIOR APPLICATION NUMBER: PCT/FI03/00946
16 <151> PRIOR FILING DATE: 2003-12-11
18 <150> PRIOR APPLICATION NUMBER: FI 20022178
19 <151> PRIOR FILING DATE: 2002-12-11
21 <160> NUMBER OF SEQ ID NOS: 6
23 <170> SOFTWARE: PatentIn version 3.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1344
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(1341)
33 <223> OTHER INFORMATION: ADRA2B variant type sequence
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38 1          5          10          15
40 gcg gcc atc acc ttc ctc att ctc ttt acc atc ttc ggc aac gct ctg      96
41 Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
42          20          25          30
44 gtc atc ctg gct gtg ttg acc agc cgc tcg ctg cgc gcc cct cag aac      144
45 Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
46          35          40          45
48 ctg ttc ctg gtg tcg ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc      192
49 Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
50          50          55          60
52 atc atc cct ttc tcg ctg gcc aac gag ctg ctg ggc tac tgg tac ttc      240
53 Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
54 65          70          75          80
56 cgg cgc acg tgg tgc gag gtg tac ctg gcg ctc gac gtg ctc ttc tgc      288
57 Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
58          85          90          95
60 acc tcg tcc atc gtg cac ctg tgc gcc atc agc ctg gac cgc tac tgg      336
61 Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp

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62	100	105	110	
64 gcc gtg agc cgc gcg ctg gag tac aac tcc aag cgc acc ccg cgc cgc	384			
65 Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg				
66 115 120 125				
68 atc aag tgc atc atc ctc act gtg tgg ctc atc gcc gcc gtc atc tcg	432			
69 Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser				
70 130 135 140				
72 ctg ccg ccc ctc atc tac aag ggc gac cag ggc ccc cag ccg cgc ggg	480			
73 Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly				
74 145 150 155 160				
76 cgc ccc cag tgc aag ctc aac cag gag gcc tgg tac atc ctg gcc tcc	528			
77 Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser				
78 165 170 175				
80 agc atc gga tct ttc ttt gct cct tgc ctc atc atg atc ctt gtc tac	576			
81 Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr				
82 180 185 190				
84 ctg cgc atc tac ctg atc gcc aaa cgc agc aac cgc aga ggt ccc agg	624			
85 Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg				
86 195 200 205				
88 gcc aag ggg ggg cct ggg cag ggt gag tcc aag cag ccc cga ccc gac	672			
89 Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp				
90 210 215 220				
92 cat ggt ggg gct ttg gcc tca gcc aaa ctg cca gcc ctg gcc tct gtg	720			
93 His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val				
94 225 230 235 240				
96 gct tct gcc aga gag gtc aac gga cac tcg aag tcc act ggg gag aag	768			
97 Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys				
98 245 250 255				
100 gag gag ggg gag acc cct gaa gat act ggg acc cgg gcc ttg cca ccc	816			
101 Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro				
102 260 265 270				
104 agt tgg gct gcc ctt ccc aac tca ggc cag ggc cag aag gag ggt gtt	864			
105 Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val				
106 275 280 285				
108 tgt ggg gca tct cca gag gat gaa gct gaa gag gag gaa gag gag gag	912			
109 Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Glu				
110 290 295 300				
112 gag gag tgt gaa ccc cag gca gtg cca gtg tct ccg gcc tca gct tgc	960			
113 Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys				
114 305 310 315 320				
116 agc ccc ccg ctg cag cag cca cag ggc tcc ccg gtg ctg gcc acc cta	1008			
117 Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu				
118 325 330 335				
120 cgt ggc cag gtg ctc ctg ggc agg ggc gtg ggt gct ata ggt ggg cag	1056			
121 Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln				
122 340 345 350				
124 tgg tgg cgt cga agg gcg cac gtg acc ccg gag aag cgc ttc acc ttc	1104			
125 Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg Phe Thr Phe				
126 355 360 365				

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128 gtg ctg gct gtg gtc att ggc gtt ttt gtg ctc tgc tgg ttc ccc ttc      1152
129 Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe
130      370      375      380
132 ttc ttc agc tac agc ctg ggc gcc atc tgc ccg aag cac tgc aag gtg      1200
133 Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val
134 385      390      395      400
136 ccc cat ggc ctc ttc cag ttc ttc ttc tgg atc ggc tac tgc aac agc      1248
137 Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser
138      405      410      415
140 tca ctg aac cct gtt atc tac acc atc ttc aac cag gac ttc cgc cgt      1296
141 Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg
142      420      425      430
144 gcc ttc cgg agg atc ctg tgc cgc ccg tgg acc cag acg gcc tgg tga      1344
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149 <210> SEQ ID NO: 2
150 <211> LENGTH: 447
151 <212> TYPE: PRT
152 <213> ORGANISM: Homo sapiens
154 <400> SEQUENCE: 2
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160 Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
161      20      25      30
164 Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
165      35      40      45
168 Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
169      50      55      60
172 Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
173 65      70      75      80
176 Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
177      85      90      95
180 Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
181      100      105      110
184 Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
185      115      120      125
188 Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
189      130      135      140
192 Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
193 145      150      155      160
196 Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
197      165      170      175
200 Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
201      180      185      190
204 Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
205      195      200      205
208 Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
209      210      215      220
212 His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val

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213 225          230          235          240
216 Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
217          245          250          255
220 Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
221          260          265          270
224 Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
225          275          280          285
228 Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu
229          290          295          300
232 Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys
233 305          310          315          320
236 Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu
237          325          330          335
240 Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln
241          340          345          350
244 Trp Trp Arg Arg Ala His Val Thr Arg Glu Lys Arg Phe Thr Phe
245          355          360          365
248 Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe
249          370          375          380
252 Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val
253 385          390          395          400
256 Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser
257          405          410          415
260 Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg
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264 Ala Phe Arg Arg Ile Leu Cys Arg Pro Trp Thr Gln Thr Ala Trp
265          435          440          445
268 <210> SEQ ID NO: 3
269 <211> LENGTH: 1353
270 <212> TYPE: DNA
271 <213> ORGANISM: Homo sapiens
273 <220> FEATURE:
274 <221> NAME/KEY: CDS
275 <222> LOCATION: (1)..(1350)
276 <223> OTHER INFORMATION: ADRA2B wild type sequence
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281 1          5          10          15
283 gcg gcc atc acc ttc ctc att ctc ttt acc atc ttc ggc aac gct ctg      96
284 Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
285          20          25          30
287 gtc atc ctg gct gtg ttg acc agc cgc tcg ctg cgc gcc cct cag aac      144
288 Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
289          35          40          45
291 ctg ttc ctg gtg tcg ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc      192
292 Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
293          50          55          60
295 atc atc cct ttc tcg ctg gcc aac gag ctg ctg ggc tac tgg tac ttc      240

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296 Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
297 65              70              75              80
299 cgg cgc acg tgg tgc gag gtg tac ctg gcg ctc gac gtg ctc ttc tgc      288
300 Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
301              85              90              95
303 acc tcg tcc atc gtg cac ctg tgc gcc atc agc ctg gac cgc tac tgg      336
304 Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
305              100              105              110
307 gcc gtg agc cgc gcg ctg gag tac aac tcc aag cgc acc ccg cgc cgc      384
308 Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
309              115              120              125
311 atc aag tgc atc atc ctc act gtg tgg ctc atc gcc gcc gtc atc tcg      432
312 Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
313              130              135              140
315 ctg ccg ccc ctc atc tac aag ggc gac cag ggc ccc cag ccg cgc ggg      480
316 Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
317 145              150              155              160
319 cgc ccc cag tgc aag ctc aac cag gag gcc tgg tac atc ctg gcc tcc      528
320 Arg Pro Gln Cys Lys Leu Asn Glu Glu Ala Trp Tyr Ile Leu Ala Ser
321              165              170              175
323 agc atc gga tct ttc ttt gct cct tgc ctc atc atg atc ctt gtc tac      576
324 Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
325              180              185              190
327 ctg cgc atc tac ctg atc gcc aaa cgc agc aac cgc aga ggt ccc agg      624
328 Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
329              195              200              205
331 gcc aag ggg ggg cct ggg cag ggt gag tcc aag cag ccc cga ccc gac      672
332 Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
333              210              215              220
335 cat ggt ggg gct ttg gcc tca gcc aaa ctg cca gcc ctg gcc tct gtg      720
336 His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
337 225              230              235              240
339 gct tct gcc aga gag gtc aac gga cac tcg aag tcc act ggg gag aag      768
340 Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
341              245              250              255
343 gag gag ggg gag acc cct gaa gat act ggg acc cgg gcc ttg cca ccc      816
344 Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
345              260              265              270
347 agt tgg gct gcc ctt ccc aac tca ggc cag ggc cag aag gag ggt gtt      864
348 Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
349              275              280              285
351 tgt ggg gca tct cca gag gat gaa gct gaa gag gag gaa gag gag gag      912
352 Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Glu
353              290              295              300
355 gag gag gag gaa gag tgt gaa ccc cag gca gtg cca gtg tct ccg gcc      960
356 Glu Glu Glu Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala
357 305              310              315              320
359 tca gct tgc agc ccc ccg ctg cag cag cca cag ggc tcc cgg gtg ctg      1008
360 Ser Ala Cys Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu

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**VERIFICATION SUMMARY**

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